logo

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NTDB id 1073 ABD1 RS00865 WP 015451369.1      MLTQLSSHHYHTLKVWYLVQHSLVSFKKIIDYFGNCEKATQPDGLAKWSSLGLHANHLKRVNEFQTT.QGQAQFEQLVQQ   79
NTDB id 1043 HON27 RS16615 WP 168727007.1     MLTQLSSHQYHTLKVWYLVQHSLVSFKKIIDYFGNCEKATQPDGLAKWSSLGLHANHLKRVNEFQTP.QGQAQFEQLVQQ   79
NTDB id 1021 ACIAD RS00975 WP 004930462.1     MITILSSHHYHTIKVWYVLQHSLSGFKKLIHYFGDCETALQPQRLSDWQKLGLHANHLKRLEEVHTL.QGQQQFEKMLAQ   79
NTDB id 1094 KZH42 RS01320 WP 002224767.1     ...MTEDERFAWLQLAFTPYIGAESFLLLMRRFGSAQNALSA.PAEQVAALIRHKQALEAWRNAEKRALARQAAEAALEW   76
NTDB id 1089 NMB RS00600 WP 002224767.1       ...MTEDERFAWLQLAFTPYIGAESFLLLMRRFGSAQNALSA.PAEQVAALIRHKQALEAWRNAEKRALARQAAEAALEW   76
NTDB id 1122 OK783 RS09595 WP 003705341.1     ...MTEDERFAWLQLAFTPYIGAESFLLLMRSFGSAQNALSA.PAEQVAPAVRHKHALEAWRNAEKRALARQAAEAALEW   76
NTDB id 1120 NGFG RS10355 WP 020997408.1      ...MTEDERFAWLQLAFTPYIGAESFLLLMRSFGSAQNALSA.PAEQVAPAVRHKHALEAWRNAEKRALARQAAEAALEW   76
NTDB id 1388 A4U84 RS04945 WP 062924099.1     .....MTHLTKLLALLQVPQLGAQRIGRLLSEVDFGEF.CQY.DKTALKQMGWNERQIQRWFNPEHK.....WIDQALQW   68
NTDB id 1361 HI 0985 AAC22646.1               ....MNDITYTLLRLMQVPKLGGVGIDKILSNITLNEL.LNY.DDVAFRQMGWGAIQIRRWFKPEAK.....FIEPALVW   69
NTDB id 1250 GCO85 RS13065 WP 027219989.1     .....MNNLQPLLALNRMKRIGPRTVLKLQK.RWPDLN.LMF....QLSSVDLEEAGLPSWLAQTIKNFDPDFIKTDLNW   69
NTDB id 1006507 ABDM36 RS00175 WP 000654772.1 ...MKDQDLAAWLALCFTPKLGSKTISHLLATRLPAQL.QSF.TPKQWLACGLKPEQLVFLTTQAAK.....QAEQCLQW   70
NTDB id 1152 A1552VC RS00200 WP 000654772.1   ...MKDQDLAAWLALCFTPKLGSKTISHLLATRLPAQL.QSF.TPKQWLACGLKPEQLVFLTTQAAK.....QAEQCLQW   70
NTDB id 1399 DSB67 RS15600 WP 010645755.1     MTPQNDIDLAAWLKLSCLPGIGGVKMNKLLSKDTPSNI.VQY.STEQLQLLGLTAKQLQAW.SQVDK.....EVDACLTW   72
consensus                                              *  *  *  *  *  **  *    **         *          *    **     *   *     *         *  *  *
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NTDB id 1073 ABD1 RS00865 WP 015451369.1      V.RQHTDFILTPDDSGYPTQLLPYTDHPPIIFGKGQAQALLQPQIAIVGSRKPSPHGRQVAYDFAYYLSEKGFFISSGLA   158
NTDB id 1043 HON27 RS16615 WP 168727007.1     V.RQHTDFILTPDDSGYPTQLLPYTDHPPIIFGKGQAQALLQPQIAIVGSRKPSPHGRQVAYDFAYYLSEKGFFISSGLA   158
NTDB id 1021 ACIAD RS00975 WP 004930462.1     L.QTHTDFIVTPDDPAYPSQLIPYQDRPPILFGQGSIQSLIQPQIAVVGSRKPSPHGRQVAYDFSYFLSEKGFYITSGLA   158
NTDB id 1094 KZH42 RS01320 WP 002224767.1     EMR.DGCRLMLLQDEDFPEMLTQGLTAPPVLFLRGNVQLLHKPSAAIVGSRHATPQAMRIAKDFGKSLGGKGIPVVSGMA   155
NTDB id 1089 NMB RS00600 WP 002224767.1       EMR.DGCRLMLLQDEDFPEMLTQGLTAPPVLFLRGNVQLLHKPSAAIVGSRHATPQAMRIAKDFGKSLGGKGIPVVSGMA   155
NTDB id 1122 OK783 RS09595 WP 003705341.1     EMR.DGCRLMLLQDEDFPEMLTQGLTAPPVLFLRGNVRLLHKPSAAIVGSRHATPQAMRIAKDFGRALGGKGIPTVSGMA   155
NTDB id 1120 NGFG RS10355 WP 020997408.1      EMR.DGCRLMLLQDEDFPEMLTQGLTAPPVLFLRGNVRLLHKPSAAIVGSRHATPQAMRIAKDFGRALGGKGIPTVSGMA   155
NTDB id 1388 A4U84 RS04945 WP 062924099.1     AEQ.DQQQILTLFDEDYPFLLKQISTAPPVLFVRGNVESLSLPQIAIVGSRDYSHYGEHWAGHFSAELVKHQLAVTSGLA   147
NTDB id 1361 HI 0985 AAC22646.1               SQK.EGNHLVNYFSPFYPFLLKQTASFPPLLFVKGNLTALSQRQMAMVGSRYCTTYGEYWAKHFATELSLAGFTITSGLA   148
NTDB id 1250 GCO85 RS13065 WP 027219989.1     LSSSENHHILTWDSPYYPALLKEIADPPFILYAKGELSALTQPSLAIVGSRNASVTGNENARAFSREISRHGVSIVSGLA   149
NTDB id 1006507 ABDM36 RS00175 WP 000654772.1 RSAANNRYIVTPHCPLYPRLLKEINSSPPVLFIEGIWEAVHDPAVAIVGSRNASVDGRQIARQFATELAQSGLVVTSGLA   150
NTDB id 1152 A1552VC RS00200 WP 000654772.1   RSAANNRYIVTPHCPLYPRLLKEINSSPPVLFIEGIWEAVHDPAVAIVGSRNASVDGRQIARQFATELAQSGLVVTSGLA   150
NTDB id 1399 DSB67 RS15600 WP 010645755.1     VAASSHHHILTLADALYPPLLKQTVAPPPLLFVKGEASCLPQPQIAMVGSRNASVDGLQHTRTFASDLVQHDLIVTSGLA   152
consensus                                              ***  *  *! *!    *  !*******!**  *  * *!*!!!! **  *  ***  !*  *    ** **!!*!
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NTDB id 1073 ABD1 RS00865 WP 015451369.1      YGIDEAAHQGASA.HQRTIAVTGTGLDTTYPAQNKKLAEYILAQNGAIITEFLPGTPPLQQHFPRRNRIVSGLSLGVLVV   237
NTDB id 1043 HON27 RS16615 WP 168727007.1     YGIDEAAHQGAST.HQRTIAVTGTGLDTTYPAQNKKLAEHILAKNGAIITEFLPGTPPLQQHFPRRNRIVSGLSLGVLVV   237
NTDB id 1021 ACIAD RS00975 WP 004930462.1     HGIDEAAHQGSLV.HHRAIAVVGTGLDLCYPSGNKALKQHIRDQGGAIVSEFLPGTPPLQAHFPRRNRIVSGLSLGVLVV   237
NTDB id 1094 KZH42 RS01320 WP 002224767.1     SGIDTAAHQGALQAEGGTIAVWGTGIDRIYPPVNKNLAYEIAE.KGLIVSEFPIGTRPYAGNFPRRNRLIAALSQVTLVV   234
NTDB id 1089 NMB RS00600 WP 002224767.1       SGIDTAAHQGALQAEGGTIAVWGTGIDRIYPPVNKNLAYEIAE.KGLIVSEFPIGTRPYAGNFPRRNRLIAALSQVTLVV   234
NTDB id 1122 OK783 RS09595 WP 003705341.1     SGIDTAAHQGALEAEGGTVAVWGTGIDRIYPPANKNLAYEIAE.KGLIVSEFPIGTRPYAGNFPRRNRLIAALSQVTLVV   234
NTDB id 1120 NGFG RS10355 WP 020997408.1      SGIDTAAHQGALEAEGGTIAVWGTGIDRIYPPANKNLAYEIAE.KGLIVSEFPIGTRPYAGNFPRRNRLIAALSQVTLVV   234
NTDB id 1388 A4U84 RS04945 WP 062924099.1     IGIDGFCHQRAANENGITIAVLGSGLDQVYPARHKKLAEQIVETSGALVSEFFPSQPPIAENFPRRNRIISGLSLGTLVI   227
NTDB id 1361 HI 0985 AAC22646.1               LGIDGHCHQAVVNIQGQTIAVLGSGLEQIYPSKHQRLSAQIIENNGALVSEFLPNQAPIAANFPRRNRIISGLSVGTLVV   228
NTDB id 1250 GCO85 RS13065 WP 027219989.1     LGIDAHAHLGCLEGGGKTIAVLGTGIDCIYPRRHLKLAEQITE.NGLLLSEFPLKSPPIAGHFPLRNRIISGLSLCILVI   228
NTDB id 1006507 ABDM36 RS00175 WP 000654772.1 LGIDGYAHDGALQAQGQTVAVLGSGLAQVYPKQHQGLAERIIA.QGALVSEFAPHTPPKADHFPRRNRIISGLSLGVVVV   229
NTDB id 1152 A1552VC RS00200 WP 000654772.1   LGIDGYAHDGALQAQGQTVAVLGSGLAQVYPKQHQGLAERIIA.QGALVSEFAPHTPPKADHFPRRNRIISGLSLGVVVV   229
NTDB id 1399 DSB67 RS15600 WP 010645755.1     LGIDGHAHDGALLAGGKTIAVLGSGLEQVYPARHRGLAQRVAE.NGALVSEFRPDAKPRAENFPRRNRIISGLSLGVLVV   231
consensus                                      !!!  *!****  *  *  **!!  !*!**  *!!    *  !*  *  *   !****!!  *  *  !  *   !!*!!!****!!**  *!*
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X non conserved
X similar
X ≥ 50% conserved